

## Appendix A

1	100													
SEQ1	(1)	-----M-----	AEETGGTNTTEAQAQPKTEAVASPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEV											
SEQ5	(1)	-----MG-----	AEETGGTNTTEAQAQPKTEAVASPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEV											
SEQ3	(1)	-----M-----	AEETGGTNTTEAQAQPKTEAVASPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEV											
SEQ4	(1)	-----MG-----	AEETGGTNTTEAQAQPKTEAVASPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEV											
SEQ28	(1)	-----MGNKQQKEFKSFYSIRKSSILGVASVAISTLLILMSNGEAQA-----	AEETGGTNTTEAQAQPKTEAVASPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEV											
Leader Sequence (amino acids 1-42) ↑														
101	200													
SEQ1	(60)	KEVKAPKETKEVKPAKATNN	TYPILNQELREAIKNPAIKDKDHSAPNSRPIDFEMKKKDG	TQQFYHYASSVKPARVIFTDSKPEIELGLQSGQFWRK	KE									
SEQ5	(61)	KEVKAPKETKEVKPAKATNN	TYPILNQELREAIKNPAIKDKDHSAPNSRPIDFEMKKKDG	TQQFYHYASSVKPARVIFTDSKPEIELGLQSGQFWRK	KE									
SEQ3	(60)	KEVKAPKETKEVKPAKATNN	TYPILNQELREAIKNPAIKDKDHSAPNSRPIDFEMKKKDG	TQQFYHYASSVKPARVIFTDSKPEIELGLQSGQFWRK	KE									
SEQ4	(61)	KEVKAPKETKEVKPAKATNN	TYPILNQELREAIKNPAIKDKDHSAPNSRPIDFEMKKKDG	TQQFYHYASSVKPARVIFTDSKPEIELGLQSGQFWRK	KE									
SEQ28	(101)	KEVKAPKETKEVKPAKATNN	TYPILNQELREAIKNPAIKDKDHSAPNSRPIDFEMKKKDG	TQQFYHYASSVKPARVIFTDSKPEIELGLQSGQFWRK	KE									
201	300													
SEQ1	(160)	VYEGDKKLPIKLVS	YD	TVKDYAIRPFSVNGTKAVKIVSSTHFN	NKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKA	KTILRQVYELN	KIQ							
SEQ5	(161)	VYEGDKKLPIKLVS	YD	TVKDYAIRPFSVNGTKAVKIVSSTHFN	NKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKA	KTILRQVYELN	KIQ							
SEQ3	(160)	VYEGDKKLPIKLVS	YD	TVKDYAIRPFSVNGTKAVKIVSSTHFN	NKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKA	KTILRQVYELN	KIQ							
SEQ4	(161)	VYEGDKKLPIKLVS	YD	TVKDYAIRPFSVNGTKAVKIVSSTHFN	NKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKA	KTILRQVYELN	KIQ							
SEQ28	(201)	VYEGDKKLPIKLVS	YD	TVKDYAIRPFSVNGTKAVKIVSSTHFN	NKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKA	KTILRQVYELN	KIQ							
301	400													
SEQ1	(260)	DKLPEKLKAEY	KKLEDT	KKALDEQVKS	AITEFQNVQPTNEKMTDLQDTKYVVY	ESVENNESMMDTFVKHP	I	KTGMLNGKKY	MMVMT	T	TNDD	YWKD	FMV	EG
SEQ5	(261)	DKLPEKLKAEY	KKLEDT	KKALDEQVKS	AITEFQNVQPTNEKMTDLQDTKYVVY	ESVENNESMMDTFVKHP	I	KTGMLNGKKY	MMVMT	T	TNDD	YWKD	FMV	EG
SEQ3	(260)	DKLPEKLKAEY	KKLEDT	KKALDEQVKS	AITEFQNVQPTNEKMTDLQDTKYVVY	ESVENNESMMDTFVKHP	I	KTGMLNGKKY	MMVMT	T	TNDD	YWKD	FMV	EG
SEQ4	(261)	DKLPEKLKAEY	KKLEDT	KKALDEQVKS	AITEFQNVQPTNEKMTDLQDTKYVVY	ESVENNESMMDTFVKHP	I	KTGMLNGKKY	MMVMT	T	TNDD	YWKD	FMV	EG
SEQ28	(301)	DKLPEKLKAEY	KKLEDT	KKALDEQVKS	AITEFQNVQPTNEKMTDLQDTKYVVY	ESVENNESMMDTFVKHP	I	KTGMLNGKKY	MMVMT	T	TNDD	YWKD	FMV	EG
401	500													
SEQ1	(360)	QVRVTISKDAKNN	TR	TIIFPVYVEGKTL	YDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQ	QDNSAKKEATPATPSKPTP	-----							
SEQ5	(361)	QVRVTISKDAKNN	TR	TIIFPVYVEGKTL	YDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQ	QDNSAKKEATPATPSKPTP	-----							
SEQ3	(360)	QVRVTISKDAKNN	TR	TIIFPVYVEGKTL	YDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQ	QDNSAKKEATPATPSKPTSP	VEKESQK	QDSQ						
SEQ4	(361)	QVRVTISKDAKNN	TR	TIIFPVYVEGKTL	YDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQ	QDNSAKKEATPATPSKPTSP	VEKESQK	QDSQ						
SEQ28	(401)	QVRVTISKDAKNN	TR	TIIFPVYVEGKTL	YDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQ	QDNSAKKEATPATPSKPTSP	VEKESQK	QDSQ						
501	600													
SEQ1	(447)	-----												
SEQ5	(448)	-----												
SEQ3	(460)	-----												
SEQ4	(461)	-----												
SEQ28	(501)	-----												
601	654													
SEQ1	(447)	-----												
SEQ5	(448)	-----												
SEQ3	(560)	KNTQENKAKS	----											
SEQ4	(561)	KNTQENKAKS	----											
SEQ28	(601)	KNTQENKAKSLPQT	GEESNKDMTLP	LMALLALSSIVAFVLP	PRKRKNLEHHHHHH									
Sortase Cleavage Site ↑														